Amendments to the Specification

Please replace the paragraph beginning on page 11, line 4-14, with the following amended paragraph:

However, in order to optimize the yield and kinetics of the PCR reaction, the desired primer sequences are also subject to other criteria. First, a primer sequence should not be substantially self-complementary or complementary to the second primer. In particular, potential primer sequences are excluded which could result in the formation of stable hybrids involving the 3' terminus of the primer and either another sequence in the same or the second primer (defined as $\geq$6 base pairs). Additionally, the T_m of one member of the primer pair should occur within 2C of its counterpart, which enables them to denature and anneal to the template nearly simultaneously. Software is well known in the art to identify primer sequences that satisfy all of the preferred criteria (see for example: ~~http://www-genome.wi.mit.edu/ftp/pub/software/primer.0.5/ or http://www.oligo.net/Oligo_6_tour.htm~~ the Oligo 6 tour located on the Broad Institute website or at oligo.net).

Please add the following paragraph to the beginning of the section entitled "BRIEF DESCRIPTION OF THE DRAWINGS" on page 4, beginning on line 23:

The patent or application file contains at least one drawing executed in color. Copies of this patent or patent application publication with color drawings will be provided by the Office upon request and payment of the necessary fee.

Please replace the paragraph beginning on page 19, line 10-25, with the following amended paragraph:

Initially, a computer-based search using the search term "HIRA" was performed using Entrez Nucleotide software at the National Library of Medicine website. This identified a series of cDNA sequences for the HIRA gene in GenBank. The full length cDNA sequence was selected (GenBank Accession No. X81844), having 3859 bp. This cDNA sequence was then compared with the genome sequence which included draft sequences at the National Library of Medicine (which can be found on the website for National Center for Biotechnological Information located at ncbi.nlm.nih.gov ~~http://www.ncbi.nlm.nih.gov/genome/seq/page.cgi?F=HsBlast.html&&ORG=Hs~~). This was done in order to determine whether genomic sequences of sufficient length were available for probe development. This comparison confirmed that the entire HIRA genomic sequence was known, and that the coding sequence interval spanned a length of 100,836 bp in the chromosome. Since the available contiguous genomic sequence in GenBank exceeded the length of the coding interval, it was possible to select an interval longer than the coding region in order to include sequences from the gene promoter at the 5' end and untranslated sequences and polyadenylation signal at the 3'end. A total genomic interval of approximately 103kb was thus selected. Position 1 of this ~103 kb interval corresponds to position 798,334 in GenBank Accession number NT_001039.